

**SEQUENCE LISTING**

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<110> Kinney, Anthony
<120> Hypoallergenic Transgenic Soybeans
<130> BB1432 US NA
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<150> 60/189,823
<151> 16 MARCH 2000

<160> 16

<170> Microsoft Office 97

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<213> chimeric construct

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<212> DNA  
<213> Glycine max

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 tctacgatg caaaaaaagcc gatccaaaaa acgccttatgg ttggagcaag gcactgcatt 900  
 gaggcgatg tccctcactc aegcaaccgg atattggat ttactgttc aaactctcag 960  
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 <211> 454  
 <212> PRT  
 <213> Glycine max

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 35 40 45  
 Met His Ile Gly Phe Ile Ser Met Glu Pro Lys Ser Leu Phe Val Pro  
 50 55 60  
 Gln Tyr Leu Asp Ser Asn Leu Ile Ile Phe Ile Arg Arg Gly Glu Ala  
 65 70 75 80  
 Lys Leu Gly Phe Ile Tyr Asp Asp Glu Leu Ala Glu Arg Arg Leu Lys  
 85 90 95  
 Thr Gly Asp Leu Tyr Met Ile Pro Ser Gly Ser Ala Phe Tyr Leu Val  
 100 105 110  
 Asn Ile Gly Glu Gly Gln Arg Leu His Val Ile Cys Ser Ile Asp Pro  
 115 120 125  
 Ser Thr Ser Leu Gly Leu Glu Thr Phe Gln Ser Phe Tyr Ile Gly Gly  
 130 135 140  
 Gly Ala Asn Ser His Ser Val Leu Ser Gly Phe Glu Pro Ala Ile Leu  
 145 150 155 160  
 Glu Thr Ala Phe Asn Glu Ser Arg Thr Val Val Glu Glu Ile Phe Ser  
 165 170 175  
 Lys Glu Leu Asp Gly Pro Ile Met Phe Val Asp Asp Ser His Ala Pro  
 180 185 190  
 Ser Leu Trp Thr Lys Phe Leu Gln Leu Lys Lys Asp Asp Lys Glu Gln  
 195 200 205

Gln Leu Lys Lys Met Met Gln Asp Gln Glu Glu Asp Glu Glu Glu Lys  
 210 215 220  
 Gln Thr Ser Arg Ser Trp Arg Lys Leu Leu Glu Thr Val Phe Gly Lys  
 225 230 235 240  
 Val Asn Glu Lys Ile Glu Asn Lys Asp Thr Ala Gly Ser Pro Ala Ser  
 245 250 255  
 Tyr Asn Leu Tyr Asp Asp Lys Lys Ala Asp Phe Lys Asn Ala Tyr Gly  
 260 265 270  
 Trp Ser Lys Ala Leu His Gly Gly Glu Tyr Pro Pro Leu Ser Glu Pro  
 275 280 285  
 Asp Ile Gly Val Leu Leu Val Lys Leu Ser Ala Gly Ser Met Leu Ala  
 290 295 300  
 Pro His Val Asn Pro Ile Ser Asp Glu Tyr Thr Ile Val Leu Ser Gly  
 305 310 315 320  
 Tyr Gly Glu Leu His Ile Gly Tyr Pro Asn Gly Ser Lys Ala Met Lys  
 325 330 335  
 Thr Lys Ile Lys Gln Gly Asp Val Phe Val Val Pro Arg Tyr Phe Pro  
 340 345 350  
 Phe Cys Gln Val Ala Ser Arg Asp Gly Pro Leu Glu Phe Phe Gly Phe  
 355 360 365  
 Ser Thr Ser Ala Arg Lys Asn Lys Pro Gln Phe Leu Ala Gly Ala Ala  
 370 375 380  
 Ser Leu Leu Arg Thr Leu Met Gly Pro Glu Leu Ser Ala Ala Phe Gly  
 385 390 395 400  
 Val Ser Glu Asp Thr Leu Arg Arg Ala Val Asp Ala Gln His Glu Ala  
 405 410 415  
 Val Ile Leu Pro Ser Ala Trp Ala Ala Pro Pro Glu Asn Ala Gly Lys  
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<211> 75  
<212> PRT  
<213> Glycine max

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Asn Leu Ala Asp Thr Tyr Arg Gly Pro Cys Phe Thr Thr Gly Ser Cys  
35 40 45

Asp Asp His Cys Lys Asn Lys Glu His Leu Leu Arg Gly Arg Cys Arg  
50 55 60

Asp Asp Phe Arg Cys Trp Cys Thr Lys Asn Cys  
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<210> 7  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: P34 gene primer

<400> 7  
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<210> 8  
<211> 30  
<212> DNA  
<213> Glycine max

<220>  
<223> Description of Artificial Sequence: P34 gene primer

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<210> 9  
<211> 701  
<212> DNA  
<213> Glycine max

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<210> 10  
<211> 119  
<212> PRT  
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20 25 30

Pro Gln Pro Ser His Val Thr Ala Leu Ile Thr Arg Pro Ser Cys Pro  
35 40 45

Asp Leu Ser Ile Cys Leu Asn Ile Leu Gly Gly Ser Leu Gly Thr Val  
50 55 60

Asp Asp Cys Cys Ala Leu Ile Gly Gly Leu Gly Asp Ile Glu Ala Ile  
65 70 75 80

Val Cys Leu Cys Ile Gln Leu Arg Ala Leu Gly Ile Leu Asn Leu Asn  
85 90 95

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<210> 11  
<211> 396  
<212> DNA  
<213> Glycine max

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gctgtcattt cggggaaaaa ggggtctgtt ggtgttactg tgaagaaagac cgggtggccc 300  
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<211> 131  
<212> PRT  
<213> Glycine max

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Gly Asn His Leu Thr His Ala Ala Ile Ile Gly Gln Asp Gly Ser Val  
20 25 30

Trp Leu Gln Ser Thr Asp Phe Pro Gln Phe Lys Pro Glu Glu Ile Thr  
35 40 45

Ala Ile Met Asn Asp Phe Asn Glu Pro Gly Ser Leu Ala Pro Thr Gly  
50 55 60

Leu Tyr Leu Gly Gly Thr Lys Tyr Met Val Ile Gln Gly Glu Pro Gly  
65 70 75 80

Ala Val Ile Arg Gly Lys Lys Gly Pro Gly Gly Val Thr Val Lys Lys  
85 90 95

Thr Gly Ala Ala Leu Ile Ile Gly Ile Tyr Asp Glu Pro Met Thr Pro  
100 105 110

Gly Gln Cys Asn Met Val Val Glu Arg Leu Gly Asp Tyr Leu Ile Asp  
115 120 125

Gln Gly Tyr  
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<210> 13

<211> 396

<212> DNA

<213> Glycine max

<400> 13

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gctgtcattt gaggaaagaa gggctctggt ggtgttactg tgaagaagac cggtgccggcc 300  
ttgtatcatggt gcatttatgtt tgaaccaatg actccaggatc aatgcaacat ggttagttgaa 360  
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<211> 131

<212> PRT

<213> Glycine max

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20 25 30

Trp Ala Gln Ser Thr Asp Phe Pro Gln Phe Lys Pro Glu Glu Ile Thr  
35 40 45

Ala Ile Met Asn Asp Phe Asn Glu Pro Gly Ser Leu Ala Pro Thr Gly  
50 55 60

Leu Tyr Leu Gly Gly Thr Lys Tyr Met Val Ile Gln Gly Glu Pro Gly  
65 70 75 80



Ile Gln Lys Leu Asn Ala Leu Lys Pro Gly Asn Arg Ile Glu Ser Glu  
 35 40 45  
 Gly Gly Leu Ile Glu Thr Trp Asn Pro Asn Asn Lys Pro Phe Gln Cys  
 50 55 60  
 Ala Gly Val Ala Leu Ser Arg Cys Thr Leu Asn Arg Asn Ala Leu Arg  
 65 70 75 80  
 Arg Pro Ser Tyr Thr Asn Gly Pro Gln Glu Ile Tyr Ile Gln Gln Gly  
 85 90 95  
 Lys Gly Ile Phe Gly Met Ile Tyr Pro Gly Cys Ser Ser Thr Phe Glu  
 100 105 110  
 Glu Pro Gln Gln Pro Gln Gln Arg Gly Gln Ser Ser Arg Pro Gln Asp  
 115 120 125  
 Arg His Gln Lys Ile Tyr Asn Ser Arg Glu Gly Asp Leu Ile Ala Val  
 130 135 140  
 Pro Thr Gly Val Ala Trp Trp Met Tyr Asn Asn Glu Asp Thr Pro Val  
 145 150 155 160  
 Val Ala Val Ser Ile Ile Asp Thr Asn Ser Leu Glu Asn Gln Leu Asp  
 165 170 175  
 Gln Met Pro Arg Arg Phe Tyr Leu Ala Gly Asn Gln Glu Gln Phe  
 180 185 190  
 Leu Lys Tyr Gln Gln Glu Gln Gly His Gln Ser Gln Lys Gly Lys  
 195 200 205  
 His Gln Gln Glu Glu Asn Glu Gly Ser Ile Leu Ser Gly Phe  
 210 215 220  
 Thr Leu Glu Phe Leu Glu His Ala Phe Ser Val Asp Lys Gln Ile Ala  
 225 230 235 240  
 Lys Asn Leu Gln Gly Glu Asn Glu Gly Glu Asp Lys Gly Ala Ile Val  
 245 250 255  
 Thr Val Lys Gly Leu Ser Val Ile Lys Pro Pro Thr Asp Glu Gln  
 260 265 270  
 Gln Gln Arg Pro Gln Glu Glu Glu Glu Glu Asp Glu Lys Pro  
 275 280 285  
 Gln Cys Lys Gly Lys Asp Lys His Cys Gln Arg Pro Arg Gly Ser Gln  
 290 295 300  
 Ser Lys Ser Arg Arg Asn Gly Ile Asp Glu Thr Ile Cys Thr Met Arg  
 305 310 315 320  
 Leu Arg His Asn Ile Gly Gin Thr Ser Ser Pro Asp Ile Tyr Asn Pro  
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 Gln Ala Gly Ser Val Thr Thr Ala Thr Ser Leu Asp Phe Pro Ala Leu  
 340 345 350

Ser Trp Leu Arg Leu Ser Ala Gly Phe Gly Ser Leu Arg Lys Asn Ala  
355 360 365

Met Phe Val Pro His Tyr Asn Leu Asn Ala Asn Ser Ile Ile Tyr Ala  
370 375 380

Leu Asn Gly Arg Ala Leu Ile Gln Val Val Asn Cys Asn Gly Glu Arg  
385 390 395 400

Val Phe Asp Gly Glu Leu Gln Glu Gly Arg Val Leu Ile Val Pro Gln  
405 410 415

Asn Phe Val Val Ala Ala Arg Ser Gln Ser Asp Asn Phe Glu Tyr Val  
420 425 430

Ser Phe Lys Thr Asn Asp Thr Pro Met Ile Gly Thr Leu Ala Gly Ala  
435 440 445

Asn Ser Leu Leu Asn Ala Leu Pro Glu Glu Val Ile Gln His Thr Phe  
450 455 460

Asn Leu Lys Ser Gln Gln Ala Arg Gln Ile Lys Asn Asn Asn Pro Phe  
465 470 475 480

Lys Phe Leu Val Pro Pro Gln Glu Ser Gln Lys Arg Ala Val Ala  
485 490 495